Re-run

#11

OIPE

RAW SEQUENCE LISTING   DATE: 08/18/2004
PATENT APPLICATION: US/09/931,701A   TIME: 12:33:20

Input Set : **N:\DA\US09931701A.raw**
Output Set: **N:\CRF4\08102004\I931701A.raw**

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   1 <110> APPLICANT: Outtrup, Helle
   2        Pedersen, Poul
   3        Sorensen, Marianne
   4 <120> TITLE OF INVENTION: Subtilase Enzymes
   5 <130> FILE REFERENCE: 10065.200-US
C-->  6 <140> CURRENT APPLICATION NUMBER: US/09/931,701A
   7 <141> CURRENT FILING DATE: 2001-08-16
   8 <160> NUMBER OF SEQ ID NOS: 9
   9 <170> SOFTWARE: PatentIn version 3.1
  11 <210> SEQ ID NO: 1
  12 <211> LENGTH: 1143
  13 <212> TYPE: DNA
  14 <213> ORGANISM: Bacillus clausii
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  16 <221> NAME/KEY: CDS
  17 <222> LOCATION: (1)..(1140)
  18 <223> OTHER INFORMATION:
  19 <221> NAME/KEY: mat_peptide
  20 <222> LOCATION: (334)..()
  21 <223> OTHER INFORMATION:
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  24      Met Asn  Lys Pro Leu Gly Lys  Ile Val Ala Ser Thr  Ala Leu Leu
  25          -110                 -105                 -100
  26      att tct gtc gct ttt agt tca tcg att gca tcg gct gct gaa gaa gca        93
  27      Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala
  28          -95                  -90                  -85
  29      aaa gaa aaa tac tta att ggc ttt aat gaa cag gaa gct gtc agt gag       141
  30      Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
  31      -80                  -75                  -70                  -65
  32      ttt gtc gaa caa gta gat gca aat aat gat gtc gcc gtt ctc tct gag       189
  33      Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
  34                       -60                  -55                  -50
  35      gaa gag gaa gtc gaa att gaa ctg ctt cat gag ttc gaa acc att ccc       237
  36      Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
  37                  -45                  -40                  -35
  38      gtt tta tca gta gag tta agc cca gaa gat gtg gat acg ctt gaa ctc       285
  39      Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
  40                  -30                  -25                  -20
  41      gat cca gcg att tct tac att gag gaa gat gta gaa gta tcg att atg       333
  42      Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
  43          -15                  -10                  -5                   -1
  44      gct cag tct gtg cca tgg gga att agc cgt gtg caa gca cct gcc gcc       381
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ENTERED

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45        Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
46        1               5                   10                  15
47        cat aac cgc gga gtg aca ggt tcc ggt gta aaa gtt gct gtt ctt gat        429
48        His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
49                    20                  25                  30
50        aca ggc att tcc gcc cat cca gac tta aat atc cgc ggc ggt gct agc        477
51        Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
52                    35                  40                  45
53        ttt gtg aca ggc gag cca acg tat caa gat ggc aat gga cac ggc acg        525
54        Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr
55                50                  55             .      60
56        cat gtg gca ggg acg att gcc gct tta aac aat tcg att ggc gtc ctt        573
57        His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
58        65                  70                  75                  80
59        ggc gta gcg cct aat gct gaa cta tac gct gtt aaa gta tta gca gcc        621
60        Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala
61                    85                  90                  95
62        aac ggc aga ggc cca gtc agc tca att gcc caa ggg ttg gaa tgg gca        669
63        Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
64                    100                 105                 110
65        gga aac aat ggc atg gac gtt gcc aac ttg agt tta gga agt cca tcg        717
66        Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
67                    115                 120                 125
68        cca agc gca acg ctt gag caa gcg gtt aat agc gct act tct aga ggc        765
69        Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
70                130                 135                 140
71        gtc ctt gtc gta gca gca act gga aac tca gga aca ggc tcc ctc gac        813
72        Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp
73        145                 150                 155                 160
74        tac cca gct cgt tat gcg aac gct atg gca gtc gga gct act gac caa        861
75        Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
76                    165                 170                 175
77        aac aac aac cgc gcc agc ttt tct cag tac gga gca ggg ctt gac att        909
78        Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
79                    180                 185                 190
80        gtt gcg cca ggt gta aac gtg cag agc aca tac cca ggt tca act tac        957
81        Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
82                    195                 200                 205
83        gct agc ttc aac ggt aca tcg atg gcg act cct cac gtt gtc ggt gta        1005
84        Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val
85                210                 215                 220
86        gca gcc ctt gta aaa caa aaa aac cca tct tgg tcc aat gta caa atc        1053
87        Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
88        225                 230                 235                 240
89        cgc aat cat cta aag aat aca gcc aca agt ttg ggt agc acg aac ttg        1101
90        Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
91                    245                 250                 255
92        tat gga agc ggg ctt gtc aat gca gaa gca gca aca cgc taa            1143
93        Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
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97  <211> LENGTH: 380
98  <212> TYPE: PRT
99  <213> ORGANISM: Bacillus clausii
100 <400> SEQUENCE: 2
101     Met Asn Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
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103     Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala
104         -95                 -90                 -85
105     Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
106     -80                 -75                 -70                 -65
107     Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
108                     -60                 -55                 -50
109     Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
110                 -45                 -40                 -35
111     Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
112             -30                 -25                 -20
113     Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
114         -15                 -10                 -5                  -1
115     Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
116     1               5                   10                  15
117     His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
118                 20                  25                  30
119     Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
120             35                  40                  45
121     Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr
122         50                  55                  60
123     His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
124     65                  70                  75                  80
125     Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala
126                     85                  90                  95
127     Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
128                 100                 105                 110
129     Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
130             115                 120                 125
131     Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
132         130                 135                 140
133     Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp
134     145                 150                 155                 160
135     Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
136                 165                 170                 175
137     Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
138             180                 185                 190
139     Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
140             195                 200                 205
141     Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val
142         210                 215                 220
143     Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
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144        225                 230                 235                 240
145        Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
146                        245                 250                 255
147        Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
148                    260                 265
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 5
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Synthetic
156 <400> SEQUENCE: 3
157        Ala Gly Lys Ala Leu
158        1                 5
160 <210> SEQ ID NO: 4
161 <211> LENGTH: 4
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Synthetic
166 <400> SEQUENCE: 4
167        Ala Gly Gly Leu
168        1
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 29
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Primer
176 <400> SEQUENCE: 5
177        aatagagctc accagcttgg acaagttgg                          29
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 32
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer
185 <400> SEQUENCE: 6
186        tttggatcca tacacaaaaa aacgctgtgc cc                      32
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 29
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Primer
194 <400> SEQUENCE: 7
195        aatagagctc accagcttgg acaagttgg                          29
197 <210> SEQ ID NO: 8
198 <211> LENGTH: 32
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RAW SEQUENCE LISTING   DATE: 08/18/2004
PATENT APPLICATION: US/09/931,701A   TIME: 12:33:20

Input Set : **N:\DA\US09931701A.raw**
Output Set: **N:\CRF4\08102004\I931701A.raw**

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199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Primer
203 <400> SEQUENCE: 8
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206 <210> SEQ ID NO: 9
207 <211> LENGTH: 275
208 <212> TYPE: PRT
209 <213> ORGANISM: Bacillus
210 <400> SEQUENCE: 9
211     Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
212     1               5                   10                  15
213     His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
214                 20                  25                  30
215     Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
216                 35                  40                  45
217     Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
218             50                  55                  60
219     Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
220     65                  70                  75                  80
221     Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
222                 85                  90                  95
223     Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
224                 100                 105                 110
225     Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
226                 115                 120                 125
227     Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
228             130                 135                 140
229     Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
230     145                 150                 155                 160
231     Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
232                 165                 170                 175
233     Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
234                 180                 185                 190
235     Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
236             195                 200                 205
237     Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
238             210                 215                 220
239     Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
240     225                 230                 235                 240
241     Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
242                 245                 250                 255
243     Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
244                 260                 265                 270
245     Ala Ala Gln
246                 275
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VERIFICATION SUMMARY   DATE: 08/18/2004
PATENT APPLICATION: · **US/09/931,701A**   TIME: 12:33:21

Input Set : **N:\DA\US09931701A.raw**
Output Set: **N:\CRF4\08102004\I931701A.raw**

L:6 M:270 C: Current Application Number differs, Wrong Format
L:22 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0